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This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1-24. (Canceled)

25. (Currently amended) A method for identifying a multimer that binds to a target molecule, the method comprising,

providing a library of polypeptides, the polypeptides comprising ~~different~~ LDL-receptor class A monomer domains, wherein the monomer domains ~~have~~ consist of 30-100 amino acids;

screening the library of polypeptides for affinity to a target molecule;

identifying at least ~~a first~~ one polypeptide comprising a first LDL-receptor class A monomer domain that specifically binds to a target molecule;

linking the first LDL-receptor class A monomer domain to a plurality of ~~different~~ additional LDL-receptor class A monomer domains to form a library of ~~different~~ LDL-receptor class A multimers, the multimers comprising the first monomer domain and one of the plurality of ~~different~~ additional monomer domains;

screening the library of multimers for the ability to bind to the target molecule; and

identifying a multimer that specifically binds to the target molecule~~, wherein the multimer comprises the first monomer domain and a second monomer domain~~.

26. (Previously presented) The method of claim 25, wherein the monomer domains comprise at least two disulfide bonds.

27. (Previously presented) The method of claim 25, wherein the monomer domains comprise six cysteines.

28. (Previously presented) The method of claim 25, wherein the identified multimer has an increased affinity for the target molecule compared to the affinity of the first monomer domain alone for the target molecule.

29. (Previously presented) The method of claim 25, wherein the target molecule is a protein.

30. (Previously presented) The method of claim 25, wherein the library of polypeptides is encoded by a library of polynucleotides and the library of polynucleotides is expressed to produce the library of polypeptides.

31. (Currently amended) The method of claim 30, wherein the library of polypeptides comprise at least 100 different polypeptides, each of the 100 different polypeptides comprising a different monomer domain consisting of ~~having~~ between 30-100 amino acids.

32. (Canceled)

33. (Previously presented) The method of claim 25, further comprising:

linking the identified multimer to a plurality of different monomer domains to form a library of trimers, each trimer comprising the first monomer domain and the second monomer domain of the identified multimer and one of the plurality of different monomer domains;

screening the library of trimers for the ability to bind to the target molecule; and

identifying a trimer that specifically binds to the target molecule.

34. (Withdrawn) A library of multimers of domains, the library comprising a plurality of different multimers, wherein the multimers comprise two monomer domains, wherein a first monomer domain is the same between different multimers and a second monomer domain is different between different multimers, and wherein the monomer domains have 30-100 amino acids.

35. (Withdrawn) The library of claim 34, wherein the monomer domains comprise at least two disulfide bonds.

36. (Withdrawn) The library of claim 34, wherein the monomer domains comprise six cysteines.

37. (Withdrawn) The library of claim 34, wherein the library is created by the first four steps of claim 25.

38. (Withdrawn) The library of claim 34, wherein the library comprises at least 100 different multimers.

39. (Withdrawn) The library of claim 38, wherein each of the 100 different multimers comprise different LDL receptor A domain variants.

40. (Withdrawn) The library of claim 34, wherein the different multimers comprise three monomer domains, wherein two monomer domains are the same between multimers in the library and a third monomer domain is different between multimers.

41. (Withdrawn) A library of different polynucleotides encoding the plurality of different multimers of claim 34.

42. (New) A method for identifying a multimer that binds to a target molecule, the method comprising,

providing a library of polypeptides, the polypeptides comprising C2 monomer domains, wherein the monomer domains consist of 30-100 amino acids;

screening the library of polypeptides for affinity to a target molecule;

identifying at least one polypeptide comprising a first C2 monomer domain that specifically binds to a target molecule;

linking the first C2 monomer domain to a plurality of additional C2 monomer domains to form a library of C2 multimers, the multimers comprising the first monomer domain and one of the plurality of additional monomer domains;

screening the library of multimers for the ability to bind to the target molecule; and

identifying a multimer that specifically binds to the target molecule.

43. (New) The method of claim 42, wherein the monomer domains comprise at least two disulfide bonds.

44. (New) The method of claim 42, wherein the monomer domains comprise six cysteines.

45. (New) The method of claim 42, wherein the identified multimer has an increased affinity for the target molecule compared to the affinity of the first monomer domain alone for the target molecule.

46. (New) The method of claim 42, wherein the target molecule is a protein.

47. (New) The method of claim 42, wherein the library of polypeptides is encoded by a library of polynucleotides and the library of polynucleotides is expressed to produce the library of polypeptides.

48. (New) The method of claim 47, wherein the library of polypeptides comprise at least 100 different polypeptides, each of the 100 different polypeptides comprising a different monomer domain consisting of between 30-100 amino acids.

49. (New) The method of claim 42, further comprising:

linking the identified multimer to a plurality of different monomer domains to form a library of trimers, each trimer comprising the first monomer domain and the second

monomer domain of the identified multimer and one of the plurality of different monomer domains;

screening the library of trimers for the ability to bind to the target molecule; and

identifying a trimer that specifically binds to the target molecule.